

Testimony of Dr. Kristian G. Andersen, PhD

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Before the Select Subcommittee on the Coronavirus
Pandemic

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Chairman Wenstrup, Ranking Member Ruiz, and members of the Select Subcommittee. I am Kristian Andersen, Professor at [Scripps Research](#). I lead several federally funded research consortia, including the [Center for Viral Systems Biology](#), the [West African Research Network for Infectious Diseases](#), and the [SEARCH Alliance in San Diego](#).

Background

I have spent most of my scientific career studying infectious diseases and have spearheaded several international collaborations focused on elucidating the origins of outbreaks, epidemics, and pandemics (1–4). This includes work describing the evolutionary history of Lassa virus (5–9) and the emergence of Ebola virus in Africa (10–15). Closer to home, our work has elucidated the origin of Zika virus in the Americas (16–20), including showing how it got to the United States and established itself in Florida (21). All of this research has been published in top peer-reviewed journals with the larger goal of making us better prepared for pandemics. Further, my laboratory has developed some of the most commonly used technologies (22–24) and software tools (23–26) that allow us to better understand viruses.

I found my passion for infectious disease research and global health while doing my PhD at Cambridge and later as a postdoc at Harvard. Originally from Denmark, I am immensely grateful for the opportunities the United States has given me, and to be part of a scientific community that is truly the best in the world. My main passion is to focus on scientific questions that are of broad interest and with global health impact. Studying the origin, spread, and evolution of viruses checks all those boxes.

It is natural to ask *why* it is important to understand the origins of pandemics. First, it is the human thing to do — when a pandemic happens, we want to know *why*. Second, this knowledge allows us to take corrective action. During an ongoing outbreak, it is critical to understand how it started, as this enables us to mitigate the impact on human health by limiting the spread of disease. Third, identifying the causes of pandemics gives us knowledge to reduce the risk of future outbreaks. This is the essence of “pandemic preparedness” — to use scientific knowledge to save lives.

Reason for the Select Subcommittee Hearing

Today, however, I am not here because the Select Subcommittee has requested my expertise on understanding the origin of the COVID-19 pandemic (25, 27–33). Nor am I here because I am an expert on pandemic preparedness. I am here because I, together with a large network of international experts, published peer-reviewed studies that go against a preferred political narrative. The title of this hearing, “[Investigating the Proximal Origin of a Cover Up](#)”, is directly targeted at our March, 2020 peer-reviewed study in *Nature Medicine* titled “*The Proximal Origin of SARS-CoV-2*” (27). It has been alleged that our paper was initiated and orchestrated



by Dr. Anthony Fauci to disprove, dismiss, and cover-up a lab origin of SARS-CoV-2 as directed at a February 1, 2020 conference call (organized and convened by Dr. Jeremy Farrar). It has also been suggested that a \$8.9 million federal "[WARN-ID](#)" grant awarded in 2020 to myself and colleagues from five different countries was a quid-pro-quo we received for changing our conclusions about the likely origin of SARS-CoV-2.

Let me categorically say that these allegations are absurd and false.

I will address both of the allegations in greater detail. First, however, it is important to understand that the conclusions stated in *Proximal Origin* were based on scientific data and analyses by a team of international scientists with extensive track records in studying virus emergence and evolution. Further, the paper was peer-reviewed by independent experts, which included several revisions, before publication. None of this work was influenced by Dr. Fauci. Any suggestion that he did is untrue — as repeatedly attested by myself and other scientists involved in the paper or conference call. This much is also clear from the many emails and Slack messages I have shared with the Select Subcommittee, as well as my nearly eight hour transcribed interview.

Our main conclusion in *Proximal Origin*, that SARS-CoV-2 likely emerged as the result of a zoonosis — i.e., a spillover from an animal host — has only been further supported by additional evidence and studies. If convincing new evidence were to be discovered that suggests the virus emerged from a lab, we would, of course, revise our conclusions. That is how science works. However, currently, no such evidence exists.

No involvement from Dr. Fauci and the March 5, 2023 Memorandum

The Select Subcommittee Republicans have stated that "[Dr. Fauci prompted the drafting of "Proximal Origins" to disprove the lab leak theory in the early days of the COVID-19 pandemic](#)." They also leveled the same charge in a Memorandum they publicly released on [March 5, 2023](#).

These statements are false and based on selective quote-mining of private emails, misrepresenting what was said. In my February 12, 2020 email to Dr. Clare Thomas, Senior Editor at the journal *Nature*, I stated: "Prompted by Jeremy Farrar [sic], Tony Fauci, and Francis Collins, Eddie Holmes, Andrew Rambaut, Bob Garry, Ian Lipkin, and myself have been working through much of the (primarily) genetic data to provide agnostic and scientifically informed hypotheses around the origins of the virus". As is clear from the email, there was no "prompting" to disprove, or dismiss, a potential "lab leak". As for the meaning of "prompted", I was referring to the fact that Drs. Farrar, Fauci, and Collins all encouraged us to look more closely at the important question of COVID-19 origins, and more specifically, our initial hypothesis that this could have been an engineered or lab-associated virus.



Wed, Feb 12, 2020 at 3:08 PM

Dear Clare,

I can only imagine you must be crazy busy at the moment! I wanted to reach out to you to see if there would be interest in receiving a commentary/hypothesis piece on the evolutionary origins of SARS-CoV-2? There has been a lot of speculation, fear mongering, and conspiracies put forward in this space and we thought that bringing some clarity to this discussion might be of interest to Nature.

Prompted by Jeremy Farrah, Tony Fauci, and Francis Collins, Eddie Holmes, Andrew Rambaut, Bob Garry, Ian Lipkin, and myself have been working through much of the (primarily) genetic data to **provide agnostic and scientifically informed hypotheses around the origins of the virus**. We are not quite finished with the writeup and we still have some loose ends, but I wanted to reach out to you to see if this might potentially be of interest? We see this more as a commentary/hypothesis, as opposed to a more long-form Letter or Article.

Best,
Kristian

February 12, 2020 email to Dr. Clare Thomas, Senior Editor at Nature.

Importantly, on a January 31, 2020 call with Dr. Fauci, where I first outlined my concerns, he told me (I am paraphrasing, as I do not remember the exact words): "if you think this virus came from a lab, you should write a scientific paper on it". Not only is this not a 'prompt' to "disprove the lab leak theory", it was specifically predicated on our initial hypothesis, which was that of a "lab leak". Dr. Fauci followed up with an email that clearly shows how seriously he took my early concerns:

Jeremy:

Fri, Jan 31, 2020 at 4:38 PM

I just got off the phone with Kristian Anderson and he related to me his concern about the Furine site mutation in the spike protein of the currently circulating 2019-nCoV. I told him that as soon as possible he and Eddie Holmes should get a group of evolutionary biologists together to examine carefully the data to determine if his concerns are validated. He should do this very quickly and if everyone agrees with this concern, they should report it to the appropriate authorities. I would imagine that in the USA this would be the FBI and in the UK it would be MI5. It would be important to quickly get confirmation of the cause of his concern by experts in the field of coronaviruses and evolutionary biology. In the meantime, I will alert my US. Government official colleagues of my conversation with you and Kristian and determine what further investigation they recommend. Let us stay in touch.

Best regards,

Tony

January 31, 2020 email From Dr. Fauci to Dr. Farrar with me in Cc.

The "disprove" part of the allegation that "Dr. Fauci prompted the drafting of "Proximal Origins" to disprove the lab leak theory in the early days of the COVID-19 pandemic" is quote-mined from a February 8, 2020 email I wrote to participants of the February 1, 2020 conference call. As before, context is critically important, as is a basic understanding of the scientific method. In the email, I stated: "... focused on trying to disprove any type of lab theory, but we are at a



crossroad where the scientific evidence isn't conclusive enough to say that we have high confidence in any of the three main theories considered".

Sat, Feb 8, 2020 at 1:15 PM

A lot of good discussion here, so I just wanted to add a couple of things for context that I think are important - and why what we're considering is far from "another conspiracy theory", but rather is taking a valid scientific approach to a question that is increasingly being asked by the public, media, scientists, and politicians (e.g., I have been contacted by Science, NYT, and many other news outlets over the last couple of days about this exact question).

To Ron's question, passage of SARS-like CoVs have been ongoing for several years, and more specifically in Wuhan under BSL-2 conditions - see references 12-15 in the document for a few examples. The fact that Wuhan became the epicenter of the ongoing epidemic caused by nCoV is likely an unfortunate coincidence, but it raises questions that would be wrong to dismiss out of hand. Our main work over the last couple of weeks has been focused on trying to *disprove* any type of lab theory, but we are at a crossroad where the scientific evidence isn't conclusive enough to say that we have high confidence in any of the three main theories considered. Like Eddie - and I believe Bob, Andrew, and everybody on this email as well - I am very hopeful that the viruses from pangolins will help provide the missing pieces. For now, giving the lab theory serious consideration has been highly effective at countering many of the circulating conspiracy theories, including HIV recombinants, bioengineering, etc. - here's just one example: <https://www.factcheck.org/2020/02/baseless-conspiracy-theories-claim-new-coronavirus-was-bioengineered/>.

As to publishing this document in a journal, I am currently not in favor of doing so. I believe that publishing something that is open-ended could backfire at this stage. I think it's important that we try to gather additional evidence - including waiting on the pangolin virus sequences and further scrutinize the furin cleavage site and O-linked glycans - before publishing. That way we can (hopefully) come out with some strong conclusive statements that are based on the best data we have access to. I don't think we are there yet.

Best,
Kristian

February 8, 2020 email from me to participants on the February 1, 2020 conference call.

In that email, I also state that it would be "wrong to dismiss [a "lab leak"] out of hand".

The scientific method, as routinely used by scientists in the United States and throughout the world, is based on two basic concepts of: (1) formulating testable hypotheses, via induction, and (2) testing those hypotheses, often via attempted falsification. My early hypothesis was that of a "lab theory" and when I stated that we were "trying to disprove any type of lab theory", I was specifically referring to the concept of falsification. This is a text-book example of the scientific method in use. As I also correctly stated in my email, however, "the scientific evidence isn't conclusive enough" to disprove a "lab leak". That was correct at the time and is correct today. We also specifically state this in *Proximal Origin*, where we said that it was (and still is) "currently impossible to prove or disprove" the origin of SARS-CoV-2 based on available evidence (27).

In their March 5, 2023 Memorandum, in addition to the points above, the Select Subcommittee Republicans state that "Only three days later, on February 4, 2020, four participants of the conference call authored a paper entitled "The Proximal Origin of SARS-CoV-2" (Proximal Origin) and sent a draft to Drs. Fauci and Collins. Prior to final publication in Nature Medicine, the paper was sent to Dr. Fauci for editing and approval". These statements are false. Our *Proximal Origin* paper was published on March 17, 2020 (45 days after the February 1, 2020



conference call), with a preprint posted on [Virological.org](https://virological.org) on February 17, 2020 (16 days after the February 1, 2020 conference call). Although Drs. Fauci and Collins were on emails containing documents that would eventually help form the basis of the *Proximal Origin* paper, they were not sent drafts or final versions of the paper for “editing and approval”, nor did they, or any other NIH official, provide any edits or suggestions on the paper.

The Select Subcommittee Republicans are referring to a March 8, 2020 email from me to Drs. Farrar, Fauci, and Collins, where I stated: “We’re still waiting for proofs, so please let me know if you have any comments, suggestions, or questions about the paper or the press release.” Note, that I say “about the paper”, not e.g., “on the paper”.

Fri, Mar 6, 2020 at 1:22 PM

Dear Jeremy, Tony, and Francis,

Thank you again for your advice and leadership as we have been working through the SARS-CoV-2 ‘origins’ paper. We’re happy to say that the paper was just accepted by Nature Medicine and should be published shortly (not quite sure when).

To keep you in the loop, I just wanted to share the accepted version with you, as well as a draft press release. We’re still waiting for proofs, so please let me know if you have any comments, suggestions, or questions about the paper or the press release.

Tony, thank you for your straight talk on CNN last night - it’s being noticed.

Best,
Kristian

March 6, 2020 email from me to Drs. Farrar, Fauci, and Collins.

Sending a copy of a paper that has been accepted and is in “proof” (i.e., at a stage where only changes directly requested by the journal can be introduced) is simply a professional courtesy, given that Drs. Farrar, Fauci, and Collins had all shown interest in our research. Similarly, thanking somebody for their “advice and leadership” during a rapidly escalating crisis (the COVID-19 pandemic), is also a common courtesy. Other than congratulating us on the paper, these individuals did not have any questions or comments on the paper. The only suggested edit was from Dr. Farrar who recommended we change a single instance of “unlikely” with “improbable”, which we did.

No Conflict of Interest

As for the WARN-ID grant, the key funding decisions were made before the pandemic and months before the February 1 conference call (34). There is no connection between the grant and the conclusions we reached about the origins of the pandemic. We applied for this grant in June 2019, and it was scored and reviewed by independent experts in November 2019. The grant awarding process is based on merit and follows an established, documented, and transparent process (35). Based on the actual timeline of this grant, it is not possible that the merit-based federal grant awarding process was influenced by a call in February, 2020.



The importance of understanding pandemic origins

Before going any further, let me reiterate that understanding the origin of the COVID-19 pandemic is an important scientific question to which we still do not have the full answer. My colleagues and I have been investigating this question since January, 2020. While I originally thought SARS-CoV-2 likely came from a lab (36), by late February, 2020 it was clear to me that the evidence all pointed (and still points) straight to the multi-billion dollar wild-life industry in China (see, section below). Even, to a single market in the large Chinese city of Wuhan called the Huanan Seafood Wholesale Market (27–31).

Following our *Proximal Origin* paper, additional studies have only further strengthened our conclusions, including:

1. The wide reach, recombinant history, and diversity of SARS-CoV-2-like viruses that can also infect humans (37–42).
2. The Huanan market had susceptible and high-risk animals for sale during the onset of the pandemic (29, 43).
3. Genetic footprints of susceptible animals were discovered within the Huanan market, in the exact areas of the market that also had the highest virus positivity rate (29, 31).
4. Early hospitalizations can be traced back to the Huanan market (44).
5. Early cases were clustered around, and in close proximity to, the Huanan market (29).
6. Excess pneumonia-related deaths first occurred in the district of Wuhan where the Huanan market is located (28).
7. Virus genomic data strongly suggests at least two zoonoses associated with the Huanan market (30).
8. There was widespread transmission of SARS-CoV-2 before the detection of the COVID-19 pandemic (45).
9. No indications of SARS-CoV-2 exposure among personnel at the Wuhan Institute of Virology prior to the start of the pandemic (46).

These are all independent assessments. While definitive proof of the origin is lacking, as is almost always the case with virus outbreaks, any theory of the origin of SARS-CoV-2 must explain all available facts. A “lab leak” scenario not only does not do that, it is directly contrary to much of the evidence we have. In my opinion, while theoretically still possible, a “lab leak” is not a plausible hypothesis for how SARS-CoV-2 emerged. A zoonosis, on the other hand, explains the data well, and is a fully supported scientific theory for SARS-CoV-2.

These findings are unsurprising, because zoonoses associated with high-risk human activities happen at immense frequency, even if they rarely lead to human outbreaks. And wet-markets, like the Huanan market, represent especially high risk situations (47, 48). Further, the scientific



evidence base for the origin of SARS-CoV-2 is as rich, and in many cases richer, than what we have for most other outbreaks (49). While the scientific community welcomes and continues to look for additional data to advance our understanding of the origin, we already have a robust foundation for a scientifically informed conclusion that SARS-CoV-2 very likely originated through the wild-life trade in China.

Pandemic origin assessment from the Intelligence Community

Our nation's Intelligence Community has been unable to reach consensus about the origins of SARS-CoV-2. The recently declassified report from the Office of the Director of National Intelligence (ODNI), however, concluded that there is no evidence to suggest this virus came from a lab. The report specifically stated (my emphasis) (50):

- “Information available to the IC indicates that some of the research conducted by the PLA and WIV included work with several viruses, including coronaviruses, but no known viruses that could plausibly be a progenitor of SARS-CoV-2”.
- “[N]o indication that the WIV’s [Wuhan Institute of Virology] pre-pandemic research holdings included SARS-CoV-2 or a close progenitor, nor any direct evidence that a specific research-related incident occurred involving WIV personnel before the pandemic that could have caused the COVID pandemic”.
- “Information available to the IC indicates that the WIV first possessed SARS-CoV-2 in late December 2019, when WIV researchers isolated and identified the virus from samples from patients diagnosed with pneumonia of unknown causes”.
- “We assess that some scientists at the WIV have genetically engineered coronaviruses using common laboratory practices. The IC has no information, however, indicating that any WIV genetic engineering work has involved SARS-CoV-2, a close progenitor, or a backbone virus that is closely related enough to have been the source of the pandemic”.
- “We do not know of a specific biosafety incident at the WIV that spurred the pandemic and the WIV’s biosafety training appears routine, rather than an emergency response by China’s leadership”.

While my co-authors and I disagree with the IC about the likelihood of possible origin scenarios for the pandemic, our overall conclusions are the same. In *Proximal Origin*, we stated that it is “currently impossible to prove or disprove” the origin of the virus and that the evidence shows that “SARS-CoV-2 is not a purposefully manipulated virus”. We also said that “we do not believe that any type of laboratory-based scenario is plausible” (27). Compare those conclusions to the declassified intelligence report: (1) “All IC agencies assess that SARS-CoV-2 was not developed as a biological weapon”, (2) “Almost all IC agencies assess that SARS-CoV-2 was not genetically engineered”, and (3) “Most agencies assess that SARS-CoV-2 was not laboratory-adapted” (50).

My changing view on the likely origin of the COVID-19 pandemic

In early 2020, I initially believed that SARS-CoV-2 could have come from the lab. Before going any further, it is important to understand that the idea of a “lab leak” is not a consistent single hypothesis, but rather several different scenarios in which the pandemic could have been linked to research activity. Importantly, most of these scenarios are mutually exclusive. For example, if one lab is suspected, then another must be excluded. It is also important to understand the difference between “possible” and “probable” (or “plausible”). Because we almost always lack proof of outbreak origins, all scenarios are possible. However, that does not mean that they are all equally probable. The latter determination requires relevant expertise and is informed by prior information and precedent, as well as data, evidence, and analyses.

There are several versions of a “lab leak” that we considered as part of our scientific studies. In the following section, I will explain how I think (and thought) about the various scenarios, as there are no formal definitions.

1. A “purposefully manipulated virus. In this scenario, a scientist would have created a virus for the purpose of creating SARS-CoV-2 with the exact properties that we observe (e.g., high transmissibility). In other words, in this scenario, a scientist intentionally created this exact virus, for example a “bioweapon”. In *Proximal Origin* we specifically use this term and state that “SARS-CoV-2 is not a purposefully manipulated virus”. Scientists simply do not have the ability to do this.

2. An engineered virus. This is a subset of the one above, however, here we do not consider whether the engineering was “purposeful” or not, and so a “bioweapon” would not fall into this category. In *Proximal Origin*, we did not directly consider this scenario, however, we state that “it is improbable that SARS-CoV-2 emerged through *laboratory manipulation*”. We also stated that SARS-CoV-2 “is not a *laboratory construct*”, referring to one of the many existing reverse-genetics systems available for studying betacoronaviruses.

3. A cultured virus. In this scenario, a virus sampled in nature was brought to a lab where it was cultured either in cells or animals. There are many reasons why such an experiment may be performed, including to “isolate” the virus from a sample (e.g., a bat), passage the virus on cells to understand its properties (e.g., can it bind to human ACE2 receptors?), or passage it in animals to e.g., look for its ability to cause disease. Some of these experiments may be done repeatedly, for example by continuous passage in cell cultures or animals. In *Proximal Origin*, we directly considered this scenario (“3. Selection during passage”), however, as we concluded, we did not, and do not, find this scenario plausible.

4. Other research-related accidents. There are other research-related accidents that some people may consider to be a “lab leak”. For example, researchers getting infected as part of

sampling bats, causing the start of a pandemic. Similarly, a contaminated sample could be brought back to the lab, where it could infect a researcher. Another example may be the 1977 influenza pandemic, which may have been associated with challenge studies as part of vaccine research (51). We did not consider any of these scenarios in *Proximal Origin*, for the simple reason that we believe that the likelihood of any of these having occurred with a novel virus, and given the evidence, is virtually zero. Further, while still equally unlikely, several of these scenarios would be the result of a zoonosis, even if associated with research activity (e.g., the infection of a scientist studying bats in the field).

5. Zoonosis. This is the spillover of a virus directly from animals, potentially via an intermediate host. We directly considered this scenario in *Proximal Origin* (“1. Natural selection in an animal host before zoonotic transfer” and “2. Natural selection in humans following zoonotic transfer”). Given precedent and available evidence, I consider a zoonosis the only plausible and supported hypothesis for the emergence of SARS-CoV-2 (specifically, scenario #1, above).

Comparison of scenarios and their level of plausibility

When comparing the various possible SARS-CoV-2 emergence scenarios it is important to remember that we are looking at a one in a lifetime event (pandemics caused by novel viruses and as severe as the COVID-19 pandemic are fortunately rare). Hence SARS-CoV-2 must be ‘special’. If it was not, it would not have caused the very pandemic we are observing (see, for example, SARS-CoV-1). This means that whenever we assess the uniqueness of this virus (e.g., its ability for efficient human-to-human transmission), there is a very large “survivorship bias”. We need to be acutely aware of this confounder.

Importantly, all research-associated scenarios are predicated on scientists successfully having managed to either: (1) directly having found the next pandemic virus via random sampling, (2) having endowed an otherwise natural virus with the exact properties that made it go pandemic, or (3) having created a pandemic virus from scratch (or based on novel, never-before reported, ‘backbones’). All of these scenarios are also predicated on those same scientists having lied about their activities, having successfully covered it all up, accidentally having infected themselves, and all of those steps having led to a pandemic linked to the very place we would expect zoonoses with novel viruses to happen — a wet market selling wild animals.

A priori, all of these scenarios are immensely less likely than the risk that the wild-life trade poses across South-East Asia and elsewhere (47, 48, 52). Via these activities, viruses constantly ‘try’ to start the next pandemic and sarbecoviruses (the subgenus SARS-CoV-1 and SARS-CoV-2 belongs to) present especially high risk (53). Add to that, the genomic, clinical, epidemiological, and environmental evidence that we have — combined with the lack of any evidence for a “lab leak”, including evidence we would expect to have found (e.g., any ‘chatter’



about a virus that could have been SARS-CoV-2, or a very close precursor, at the Wuhan Institute of Virology prior to the pandemic) — and the likelihood, in my opinion, of a “lab leak” goes from “plausible” to “unlikely” to “not plausible”.

A brief timeline of my view of the origin

Based on limited data, preliminary analyses, and the fact that while I am an expert on investigating virus emergence and evolution, I was not an expert on coronaviruses, I initially observed features in SARS-CoV-2 that made me suspicious of a lab origin. This suspicion was furthered by the type of research ongoing at the Wuhan Institute of Virology, which included both culturing and engineering of coronaviruses. The fact that this work was ongoing was well-known and published in several peer-reviewed papers (e.g., (54–60)).

Hi Tony,

Fri, Jan 31, 2020 at 7:32 PM

Thanks for sharing. Yes, I saw this earlier today and both Eddie and myself are actually quoted in it. It's a great article, but the problem is that our phylogenetic analyses aren't able to answer whether the sequences are unusual at individual residues, except if they are completely off. On a phylogenetic tree the virus looks totally normal and the close clustering with bats suggest that bats serve as the reservoir. The unusual features of the virus make up a really small part of the genome (<0.1%) so one has to look really closely at all the sequences to see that some of the features (potentially) look engineered.

We have a good team lined up to look very critically at this, so we should know much more at the end of the weekend. I should mention that after discussions earlier today, Eddie, Bob, Mike, and myself all find the genome inconsistent with expectations from evolutionary theory. But we have to look at this much more closely and there are still further analyses to be done, so those opinions could still change.

Best,
Kristian

January 31, 2020 email from me to Dr. Fauci.

Based on my early analyses I had not yet seen several features in SARS-CoV-2 I found ‘peculiar’ in other, related, viruses. These features included a furin cleavage site that allows the SARS-CoV-2 spike protein to be easily cleaved and a version of the receptor binding domain that was different from SARS-CoV-1 but appeared to be a good binder of human ACE2.

Combined, this initially made me believe that SARS-CoV-2 could have been an engineered virus (definition #2, above — I never considered definition #1 to be plausible), which is clear in my January 31, 2020 email to Dr. Fauci.

It has been alleged, including by the Select Subcommittee Republicans, that I changed my mind from “definitely lab leak” to dismissing the lab leak as a conspiracy theory in the matter of just a few days, and that the only intervening occurrence was the February 1, 2020 conference call. This is, as I have repeatedly stated, false. To support this false allegation, a February 4, 2020 email that I wrote following a February 3, 2020 conference call organized by the National Academy of Science and Engineering (NASEM), after a request from the White House Office of Science and Technology Policy, is often brought up.



Tue, Feb 4, 2020 at 9:05 AM

I too agree with all that has been said, but would caution against adding language suggesting that the virus might evolve (i.e., "mutate" to most people) towards better infectivity or transmission - a lot has been said about that for Ebola and other viruses, and it's been driving fear because most people don't fully understand what it means. I'm not arguing that it's not something that might well happen - the SARS data beautifully show it - but I would be worried about the message it could send.

Reading through the letter I think it's great, but I do wonder if we need to be more firm on the question of engineering. The main crackpot theories going around at the moment relate to this virus being somehow engineered with intent and that is demonstrably not the case. Engineering can mean many things and could be done for either basic research or nefarious reasons, but the data conclusively show that neither was done (in the nefarious scenario somebody would have used a SARS/MERS backbone and optimal ACE2 binding as previously described, and for the basic research scenario would have used one of the many already available reverse genetic systems). If one of the main purposes of this document is to counter those fringe theories, I think it's very important that we do so strongly and in plain language ("consistent with" [natural evolution] is a favorite of mine when talking to scientists, but not when talking to the public - especially conspiracy theorists).

Best,
Kristian

February 4, 2020 email from me to participants on a February 3, 2020 conference call.

This email has been used, including by the Select Subcommittee Republicans, to allege that I started dismissing the "lab leak" as a "crackpot theory" only a few days after the February 1, 2020 conference call. This is clearly not the case, as can be seen from the email itself. The NASEM conference call had been set up because of a January 31, 2020, and now retracted, preprint on the bioRxiv titled "*Uncanny similarity of unique inserts in the 2019-nCoV spike protein to HIV-1 gp120 and Gag*" (61). That preprint resulted in many conspiracy theories that SARS-CoV-2 was e.g., a bioweapon or otherwise engineered with intent (definition #1, above). I have always considered, and still consider, that to be a "crackpot" theory.

What is clear from that email, however, is the fact that my view on "engineering" (definition #2, above) had changed after just a few days. That is also clear from the emails and Slack messages I have provided the Select Subcommittee. As I specifically stated in my January 31, 2020 email to Dr. Fauci (see, above) the "engineering" hypothesis was a conclusion that could change in just a couple of days, and it did.

As outlined in our *Proximal Origin* paper (27), this was based on several considerations, including the realization that the features in SARS-CoV-2 that initially suggested possible engineering can readily be found in related coronaviruses. I had also realized that the furin cleavage site was suboptimal and had not been used for experimentation with coronaviruses. The 'backbone' of the virus itself was also clearly novel, and, in general, the virus genome did not look like the product of engineering, but rather looked like a perfect example of a naturally evolved virus.

However, despite my dismissal of an "engineering" hypothesis, I still believed that "culturing" (definition #3, above) was a plausible scenario for the emergence of SARS-CoV-2. A view that I

kept until mid/end February, 2020, including by the time we submitted our manuscript for consideration at *Nature* and as a [preprint](#). For example, in that version of the manuscript, we do not include the sentence “we do not believe that any type of laboratory-based scenario is plausible”, which was added during revision of the paper with *Nature Medicine*. Specifically, in that version we concluded that:

“Although genomic evidence **does not support the idea** that SARS-CoV-2 is a laboratory construct, **it is currently impossible to prove or disprove** the other theories of its origin described here, and it is unclear whether future data will help resolve this issue.”

By the time we published our final version of *Proximal Origin*, however, I no longer believed that a “culturing” scenario was plausible. As is almost always the case in science, this change in belief was not based on a single piece of evidence, but a combination of many factors, including additional data, analyses, learning more about coronaviruses, and discussions with colleagues and collaborators. It is beyond the scope of this testimony to detail all of these factors, and we have thoroughly documented why we believe SARS-CoV-2 is a natural virus in our reports and peer-reviewed scientific publications (27–31).

Politicization of scientific questions and targeting of scientists

Unfortunately, the important scientific question of the origin of the COVID-19 pandemic has been contorted by politics, while scientific discourse has been abandoned in pursuit of a preferred, coordinated narrative. The attacks directed against science and scientists are reckless and the effects, far-reaching. In the light of land-use change, population expansion, and climate change, the risk of devastating pandemics caused by novel and emerging pathogens is real and ever-increasing. We need more research and commitment to science, not less, to better prepare for them. However, scientists, including myself, who dedicate their professional lives to critically impactful research are being targeted and used as pawns in a political game. While asking the question “might this virus have come from a lab?” is a natural and reasonable one to ask — and one asked (and believed) by many people acting in good faith — at this point it is not supported by scientific evidence, and most, albeit not all, of the “lab leak” narratives are being fueled by conspiracy theories and political narratives.

Taking a complete look at all the facts, peer-reviewed scientific literature must be given appropriate weight in comparison to speculation and baseless narratives. The breadcrumbs of the origin of COVID-19 lead us directly to the doorstep of a single market in central China that was selling illegal wild-life in late 2019. I suggest we start there.

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PRESS RELEASE

The Scripps Research Institute To Pay \$10 Million To Settle False Claims Act Allegations Related To Mischarging NIH-Sponsored Research Grants

Friday, September 11, 2020

For Immediate Release

Office of Public Affairs

The Scripps Research Institute (TSRI) has agreed to pay the U.S. \$10 million to settle claims that it improperly charged NIH-funded research grants for time spent by researchers on non-grant related activities such as developing, preparing, and writing new grant applications, teaching, and engaging in other administrative activities, the Department of Justice announced today.

"The NIH has finite resources to support important research across the nation," said Acting Assistant Attorney General Jeffrey Clark for the Department of Justice's Civil Division. "Today's settlement demonstrates our commitment to protect those resources by ensuring that NIH grants funds are used for the purposes for which they were intended."

"Federal grant recipients must use the grant funds they receive on tasks that specifically relate to the funded project. Those that improperly charge the government for costs unrelated to the project must be held accountable," said U.S. Attorney Robert K. Hur. "The U.S. Attorney's Office and the Department of Justice have a duty to protect government resources and ensure they are used appropriately."

EXHIBIT 4

"Taxpayers funds for medical research are finite and the need for scientific advances is great; therefore, it's critical that these resources are used as intended," said Special Agent in Charge Maureen R. Dixon, U.S. Department of Health and Human Services Office of Inspector General. "Working with our law enforcement partners, our investigators will continue to protect these resources so that they are spent appropriately."

TSRI is a non-profit biomedical research institute with campuses located in Jupiter, Florida and La Jolla, California. TSRI receives millions of dollars in funding from NIH through hundreds of grants each year. The settlement resolves allegations that between 2008 and 2016, TSRI failed to have a system in place for its faculty to properly account for time spent on activities that cannot be charged directly to NIH-funded projects or are unrelated to the research activities of the NIH-funded project. Consequently, the U.S. contended that TSRI improperly charged time spent by faculty on developing, preparing, and writing new grant applications directly to existing NIH-funded projects, rather than allocating such charges as indirect costs. The U.S. also alleged that TSRI improperly charged NIH-funded projects for time spent by its faculty on other activities unrelated to the funded projects, such as teaching, TSRI committee work, and other administrative tasks.

The settlement resolves allegations originally brought in a lawsuit filed under the *qui tam*, or whistleblower, provisions of the False Claims Act by Thomas Burris, Ph.D, a former TSRI employee. The act permits private parties to sue on behalf of the government for false claims for government funds and to receive a share of any recovery. Dr. Burris will receive \$1.75 million.

The settlement was the result of a coordinated effort by the Civil Division of the Department of Justice, the U.S. Attorney's Office for the District of Maryland, and the Office of Inspector General of the Department of Health and Human Services.

The case is captioned *U.S. ex rel. Burris v. The Scripps Research Institute*, Case No. 1:15-CV-01443 (D. Md.). The claims resolved by the settlements are allegations only; there has been no determination of liability.

Updated September 11, 2020

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FALSE CLAIMS ACT

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